In the Claims:

Please add the following claims:

65. (New) An isolated nucleic acid molecule encoding a splice variant of a reference human telomerase, wherein the reference human telomerase has regions α (encoded by 36 bases located at nucleotides 2131-2166 of Figure 1) and β (encoded by 182 bases located at nucleotides 2286-2468 of Figure 1).

66. (New) The nucleic acid molecule of claim 65, wherein the splice variant of human telomerase lacks nucleotide sequence encoding RTase motifs A, B, C, and D.

67. (New) The nucleic acid molecule of claim 65, wherein the splice variant of human telomerase lacks nucleotide sequence encoding RTase motif A.

68. (New) The nucleic acid molecule of any one of claims 65-67, wherein the splice variant of human telomerase lacks nucleotide sequence encoding a P-loop motif.

69. (New) The nucleic acid molecule of any one of claims 65-68, wherein the splice variant of human telomerase lacks the C-terminal domain of the reference human telomerase.

70. (New) The nucleic acid molecule of any one of claims 65-69, wherein the splice variant of human telomerase has an altered C-terminus comprising sequence encoding a consensus SH3 binding site.

71. (New) The nucleic acid molecule of claim 65, wherein the nucleic acid molecule comprises one of the sequences presented in Figure 11 (SEQ ID Nos: 34, 36, 38, 41, 43, 45, 47, 49, 51, 55, 63, 67, 71, 75, 79, 83), a complement thereof, or a sequence that

hybridizes under normal stringency conditions to the sequence or its complement.

72. (New) The nucleic acid molecule of claim 65, wherein the nucleic acid molecule encodes one of the amino acid sequences presented in Figure 11 (SEQ ID Nos: 35, 37, 39, 42, 44, 46, 48, 50, 52-54, 56-58, 60-62, 64-66, 68-70, 72-74, 76-78, 80-82, 84-86), or variant thereof.

73. (New) The complement of the nucleic acid molecule of claim 65.

74. (New) The nucleic acid molecule of claim 65, wherein said molecule is a DNA molecule.

75. (New) The nucleic acid molecule of claim 65, wherein said molecule is an RNA or cDNA molecule.

76. (New) An expression vector, comprising a promoter operably linked to the nucleic acid molecule according to claim 65.

77. (New) The expression vector of claim 76, wherein the vector is selected from the group consisting of bacterial vectors, retroviral vectors, adenoviral vectors and yeast vectors.

78. (New) A host cell containing a vector according to claim 76.

79. (New) The host cell of claim 78, wherein the cell is selected from the group consisting of human cell, monkey cell, mouse cell, rat cell, yeast cell and bacterial cell.

80. (New) An isolated nucleic acid molecule comprising of any of the sequences presented in Figure 10 (SEQ ID Nos: 18, 23, 25, 27, 29, 30, 32, 33), or a complement

of one of the sequences, or a variant of the sequences or complements thereof.

81. (New) An isolated nucleic acid molecule encoding any of the amino acid sequences in SEQ ID Nos. 24, 26, 28, and 31 or variant thereof

82. (New) An expression vector, comprising a promoter operably linked to the nucleic acid molecule according to claim 81.

83. (New) The expression vector of claim 82, wherein the vector is selected from the group consisting of bacterial vectors, retroviral vectors, adenoviral vectors and yeast vectors.

84. (New) A host cell containing a vector according to claim 83.

85. (New) The host cell of claim 84, wherein the cell is selected from the group consisting of human cell, monkey cell, mouse cell, rat cell, yeast cell and bacterial cell.

86. (New) An oligonucleotide comprising 15-100 contiguous nucleotides of one of the sequences presented in Figure 10 (SEQ ID Nos: 18, 23, 25, 27, 29, 30, 32, 33) or the complements thereof.

87. (New) The oligonucleotide of claim 86, wherein the oligonucleotide is from 15 to 36 nucleotides long.

88. (New) The oligonucleotide of claim 86, wherein the oligonucleotide is from 20 to 50 nucleotides long.

89. (New) The oligonucleotide of claim 86, wherein the oligonucleotide is labeled.

90. (New) The oligonucleotide of claim 89, wherein the label is a radiolabel, a chemiluminescent label, or biotin.

91. (New) A pair of oligonucleotide primers that amplify sequence selected from the group consisting of region 1 (SEQ ID No: 23), region α (SEQ ID No: 25), region β (SEQ ID No: 27), region 2 (SEQ ID No: 29), region 3 (SEQ ID No: 30), region X (SEQ ID No: 32) or region Y (SEQ ID No: 18).

92. (New) A pair of oligonucleotide primers that amplify sequence of human telomerase containing a splice junction, wherein the primer pair flanks nucleotide 222, 1950, 2131-2166, 2287-2468, 2843, or 3157 as presented in Figure 1 (SEQ ID No: 1).

93. (New) A pair of oligonucleotide primers that amplify sequence of human telomerase containing a splice junction, wherein only one primer of each primer pair flanks nucleotide 222, 1950, 2131-2166, 2287-2468, 2843, or 3157 as presented in Figure 1 (SEQ ID No: 1) and the other primer of the pair has sequence corresponding to all or a portion of one of the sequences presented in Figure 10 (SEQ ID Nos: 18, 23, 25, 27, 29, 30, 32, 33) or complements thereof.

94. (New) A method of diagnosing cancer in a patient, comprising preparing tumor cDNA and amplifying the tumor cDNA using a pair of oligonucleotide primers that amplify sequence selected from the group consisting of region 1 (SEQ ID No: 23), region α (SEQ ID No: 25), region β (SEQ ID No: 27), region 2 (SEQ ID No: 29), region 3 (SEQ ID No: 30), region X (SEQ ID No: 32) or region Y (SEQ ID No: 18), wherein the pattern of amplification is indicative of a diagnosis of cancer.

95. (New) A method of diagnosing cancer in a patient, comprising preparing tumor cDNA and amplifying the tumor cDNA using a pair of oligonucleotide primers that amplify sequence of human telomerase containing a splice junction, wherein the primer pair

flanks nucleotide 222, 1950, 2131-2166, 2287-2468, 2843, or 3157 as presented in Figure 1 (SEQ ID No: 1), wherein the pattern of amplification is indicative of a diagnosis of cancer.

96. (New) A method of diagnosing cancer in a patient, comprising preparing tumor cDNA and amplifying the tumor cDNA using a pair of oligonucleotide primers that amplify sequence of human telomerase containing a splice junction, wherein only one primer of each primer pair flanks nucleotide 222, 1950, 2131-2166, 2287-2468, 2843, or 3157 as presented in Figure 1 (SEQ ID No: 1) and the other primer of the pair has sequence corresponding to all or a portion of one of the sequences presented in Figure 10 (SEQ ID Nos: 18, 23, 25, 27, 29, 30, 32, 33) or complements thereof.

97. (New) A method of determining a pattern of telomerase RNA expression in cells, comprising,

preparing cDNA from mRNA isolated from the cells,

amplifying the cDNA using primers that amplify a splice variant of nucleic acid encoding human telomerase and

detecting the amplified product by hybridization with all or part of the sequence of region 1 (SEQ ID No: 23), all or part of the sequence of region α (SEQ ID No: 25), all or part of the sequence of region β (SEQ ID No: 27), all or part of the sequence of region 2 (SEQ ID No: 29), all or part of the sequence of region 3 (SEQ ID No: 30), all or part of the sequence of region X (SEQ ID No: 32) or all or part of the sequence of region Y (SEQ ID No: 18);

therefrom determining the pattern of telomerase RNA expression.

98. (New) A method of diagnosing cancer in a patient by determining a pattern of telomerase RNA expression, comprising,

amplifying sequence of human telomerase from cDNA synthesized from tumor RNA using primers that amplify a splice variant of human telomerase, and

detecting the amplified product by hybridization with all or part of the sequence of region 1 (SEQ ID No: 23), all or part of the sequence of region α (SEQ ID No: 25), all or part

of the sequence of region β (SEQ ID No: 27), all or part of the sequence of region 2 (SEQ ID No: 29), all or part of the sequence of region 3 (SEQ ID No: 30), all or part of the sequence of region X (SEQ ID No: 32) or all or part of the sequence of region Y (SEQ ID No: 18),

therefrom determining the pattern of telomerase RNA expression, wherein the pattern is indicative of a diagnosis of cancer.

99. (New) The method of claim 98, further comprising comparing the pattern to a pattern obtained from a reference cancer.

100. (New) A nucleic acid molecule encoding a human telomerase that lacks RTase motifs A, B, C, and D.

101. (New) A nucleic acid molecule encoding a human telomerase that lacks RTase motif A.

102. (New) The nucleic acid molecule of either of claims 101 or 102, wherein the human telomerase lacks a P-loop motif.

103. (New) The nucleic acid molecule of either of claims 101 or 102, wherein the human telomerase has an altered C-terminal domain comprising a consensus SH3 binding site.

104. (New) The nucleic acid molecule of either one of claims 102 or 103, wherein the human telomerase lacks the C-terminal domain of the human telomerase presented in SEQ ID No. 2.

105. (New) A nucleic acid molecule encoding a human telomerase that lacks a P-loop motif.

106. (New) A nucleic acid molecule encoding a human telomerase that has an